Box sequence
08 447118

SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: Burkly, Linda C.
        (B) STREET: 34 Winthrop Street
        (C) CITY: West Newton
        (D) STATE: Massachusetts
        (E) COUNTRY: USA
        (F) POSTAL CODE (ZIP): 02165

        (A) NAME: Biogen, Inc.
        (B) STREET: Fourteen Cambridge Center
        (C) CITY: Cambridge
        (D) STATE: Massachusetts
        (E) COUNTRY: USA
        (F) POSTAL CODE (ZIP): 02142

    (ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES

    (iii) NUMBER OF SEQUENCES: 15

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

    (v) CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US 000000 (BGP-151CP)
    (vi) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: PCT/US94/01456
        (B) FILING DATE: 09-FEB-1994
    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/029,330
        (B) FILING DATE: 09-FEB-1993

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 360 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..360

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1

(D) OTHER INFORMATION:/note= "pBAG159 insert: HP1/2 heavy
        chain variable region; amino acid 1 is Glu (E) but
        Gln(Q) may be substituted"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA        48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1            5                10                15

GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT        96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
             20                25                30

ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA       144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
         35                40                45

AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG       192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
     50                55                60

GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG       240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65                70                75                80

CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA       288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                 85                90                95

GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA       336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
             100               105               110

GGG ACC ACG GTC ACC GTC TCC TCA                                       360
Gly Thr Thr Val Thr Val Ser Ser
         115               120
```

(2) INFORMATION FOR SEQ ID NO: 2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 120 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1            5                10                15

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
             20                25                30

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
         35                40                45
```

```
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
    50              55                  60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
65              70                  75                  80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            85                  90                  95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
            100             105             110

Gly Thr Thr Val Thr Val Ser Ser
        115             120
```

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 318 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..318
        (D) OTHER INFORMATION:/product= "HP1/2 light
            chain variable region"

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 1
        (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2 light
            chain variable region"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA        48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
            125             130             135

GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT        96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
            140             145             150

GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA       144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
            155             160             165

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC       192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    170             175             180

AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT       240
```

```
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
185             190             195             200

GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC        288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
                205             210             215

ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC                               318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            220             225
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 106 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1               5               10              15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
            20              25              30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35              40              45

Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
    50              55              60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65              70              75              80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
            85              90              95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100             105
```

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 429 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT          48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19            -15             -10                 -5

GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA          96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
               1               5               10

CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT         144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
    15              20              25

AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT         192
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30              35              40                  45

GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC         240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
               50              55              60

CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC         288
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
           65              70              75

CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC         336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
        80              85              90

TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC         384
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
    95              100             105

TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC             429
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110             115             120
```

(2) INFORMATION FOR SEQ ID NO: 6:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 143 amino acids

(B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19             -15             -10                 -5

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
            1               5                   10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
    15              20              25

Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30              35              40                      45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
            50              55              60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
        65              70              75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
        80              85              90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
    95              100             105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110             115             120
```

(2) INFORMATION FOR SEQ ID NO: 7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 386 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..386

    (ix) FEATURE:
            (A) NAME/KEY: sig_peptide
            (B) LOCATION: 1..57

    (ix) FEATURE:
            (A) NAME/KEY: mat_peptide
            (B) LOCATION: 58..386

    (ix) FEATURE:
            (A) NAME/KEY: misc_feature

```
        (B) LOCATION: 1
        (D) OTHER INFORMATION:/note= "pBAG198 insert: VK2
            (SVMDY) light chain variable region"


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT         48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19             -15                 -10                     -5

GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC         96
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
                1               5                   10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG        144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
        15                  20                  25

ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG        192
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 30                 35                  40                      45

CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA        240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
                50                  55                  60

TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC        288
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
            65                  70                  75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC        336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
        80                  85                  90

TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG        384
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
    95                  100                 105

TG                                                                      386


(2) INFORMATION FOR SEQ ID NO: 8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 128 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19             -15                 -10                     -5

Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
                1               5                   10
```

```
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
    15              20              25

Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30              35              40              45

Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
            50              55              60

Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
            65              70              75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
        80              85              90

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
    95              100             105
```

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1347 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..1338

    (ix) FEATURE:
        (A) NAME/KEY: VCAM-1 gene segment
        (B) LOCATION: 1..219
        (D) OTHER INFORMATION: This portion of the sequence
            corresponds, in part, to Exons I, II and III
            nucleotide sequence of Cybulsky et al. Proc. Nat'l.
            Acad. Sci. USA 88: 7861(1991).

    (ix) FEATURE:
        (A) NAME/KEY: Hinge region
        (B) LOCATION: 220..229
        (D) OTHER INFORMATION: This portion of the sequence
            corresponds, in part, to Fig. 12A in PCT/US92/02050
            and represents the hinge region of Human IgG1 heavy
            chain constant region.

    (ix) FEATURE:
        (A) NAME/KEY: Heavy chain constant region 2
        (B) LOCATION: 230..338
        (D) OTHER INFORMATION: This portion of the sequence
            corresponds, in part, to Fig. 12A in PCT/US92/02050
            and represents the heavy chain constant region 2 of
            Human IgG1 heavy chain constant region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG        48
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
110             115             120             125

ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA        96
Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
                130             135             140

TCT AGA TAT CTT GCT CAG ATT GGT GAC TCC GTC TCA TTG ACT TGC AGC       144
Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
            145             150             155

ACC ACA GGC TGT GAG TCC CCA TTT TTC TCT TGG AGA ACC CAG ATA GAT       192
Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
            160             165             170

AGT CCA CTG AAT GGG AAG GTG ACG AAT GAG GGG ACC ACA TCT ACG CTG       240
Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
            175             180             185

ACA ATG AAT CCT GTT AGT TTT GGG AAC GAA CAC TCT TAC CTG TGC ACA       288
Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
190             195             200             205

GCA ACT TGT GAA TCT AGG AAA TTG GAA AAA GGA ATC CAG GTG GAG ATC       336
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
            210             215             220

TAC TCT TTT CCT AAG GAT CCA GAG ATT CAT TTG AGT GGC CCT CTG GAG       384
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
            225             230             235

GCT GGG AAG CCG ATC ACA GTC AAG TGT TCA GTT GCT GAT GTA TAC CCA       432
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
            240             245             250

TTT GAC AGG CTG GAG ATA GAC TTA CTG AAA GGA GAT CAT CTC ATG AAG       480
Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
            255             260             265

AGT CAG GAA TTT CTG GAG GAT GCA GAC AGG AAG TCC CTG GAA ACC AAG       528
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
270             275             280             285

AGT TTG GAA GTA ACC TTT ACT CCT GTC ATT GAG GAT ATT GGA AAA GTT       576
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
            290             295             300
```

```
CTT GTT TGC CGA GCT AAA TTA CAC ATT GAT GAA ATG GAT TCT GTG CCC        624
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
            305             310             315

ACA GTA AGG CAG GCT GTA AAA GAA TTG CAA GTC GAC AAA ACT CAC ACA        672
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr
            320             325             330

TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC        720
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
            335             340             345

CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT        768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
350             355             360             365

GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC        816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            370             375             380

AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA        864
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            385             390             395

AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC        912
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            400             405             410

CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC        960
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
            415             420             425

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC        1008
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
430             435             440             445

AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA        1056
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            450             455             460

TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC        1104
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            465             470             475

AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG        1152
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            480             485             490

CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC        1200
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            495             500             505

GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG        1248
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
510             515             520             525

CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC        1296
```

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
              530   535   540

AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA   1338
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
          545   550   555

TGAGTGCGG   1347

(2) INFORMATION FOR SEQ ID NO: 10:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 24 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (ix) FEATURE:
             (A) NAME/KEY: CDS
             (B) LOCATION: 6..23
             (D) OTHER INFORMATION: This corresponds to Kinase
                     Primer 370-31.

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCGTC GAC AAA ACT CAC ACA TGC C   24
      Asp Lys Thr His Thr Cys
       1   5

(2) INFORMATION FOR SEQ ID NO: 11:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 24 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (ix) FEATURE:
             (A) NAME/KEY:
             (B) LOCATION:
             (D) OTHER INFORMATION: This corresponds to Kinase
                     Primer 370-32.

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTAAATGAGT GCGGCGGCCG CCAA   24

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 115 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG ATCTGCAGCA   60

TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC   115

(2) INFORMATION FOR SEQ ID NO: 13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 41 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 21..41

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GAGCTCGAGG CGGCCGCACC ATG CCT GGG AAG ATG GTC GTG   41
                      Met Pro Gly Lys Met Val Val
                      1   5

(2) INFORMATION FOR SEQ ID NO: 14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

(2) INFORMATION FOR SEQ ID NO: 15:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 14 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCGACGCGGC CGCG   14